Amendments to the Claim:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 (currently amended). A method of combinatorially generating a second or higher level library comprising a plurality of library members, said members including a plurality of different glycopeptides, including glycopeptides comprising at least one carbohydrate structure comprising at least two sugar units, comprising the steps of :

(a) providing at least one first level library, each library comprising a plurality of first level library members, said first level library members including a plurality of different glycopeptides, said glycopeptides each comprising a core peptide and at least one carbohydrate structure comprising at least one sugar unit, said glycopeptides being diversely glycosylated, where at least one carbohydrate structure of each of said glycopeptides provides at least one unblocked second level glycosylation site, such that reaction with a glycosyl donor at that site results in extension of said carbohydrate structure by at least one sugar unit, and

(b) randomly glycosylating said first level library by reacting the library with a mixture of at least two different glycosyl donors, thereby ~~enlarging~~ extending one or more ~~the~~ carbohydrate structures of a plurality of said first level library glycopeptides whereby a second level library, comprising a plurality of second level library members, is generated, said members comprising a plurality of glycopeptides, and including glycopeptides comprising at least one carbohydrate structure comprising at least two sugar units, said glycopeptides collectively providing ~~glycopeptides of~~ greater carbohydrate diversity, is created

where said core peptide is the core peptide of mucin-1 (MUC1), or of a fragment of MUC1, at least four amino acids in length, which comprises at least one N- or O-glycosylation site.

2 (previously presented). A method according to claim 1, which further comprises further randomly glycosylating said second level library to produce a higher level library of further increased carbohydrate diversity.

3 (previously presented). A method according to claim 49, wherein said core peptide comprises the amino acid sequence (SEQ ID NO: 1) GVTSAPDTRPAPGSTA.

4 (previously presented). A method according to claim 49, wherein said core peptide comprises the amino acid sequence (SEQ ID NO: 2) GSTA.

5 (previously presented). A method according to claim 44, wherein glycosylation sites which did not react with a glycosyl donor in step (a') are blocked prior to step (b).

6 (previously presented). A method according to claim 5, wherein said sites are blocked by acetylation.

7 (original). A method according to claim 3, wherein said glycosyl donors are selected from the group consisting of GalNAc, βGal(1-3)αGalNAc and sialyl.

8 (original). A method according to claim 4, wherein said glycosyl donors are selected from the group consisting of GalNAc, βGal(1-3)αGalNAc and sialyl.

9 (previously presented). A method according to claim 1, wherein hydroxyl groups on said glycosyl donors are protected prior to reaction of said glycosyl donors with said glycopeptides.

10 (previously presented). A method according to claim 9, wherein said hydroxyl groups are deprotected after reaction glycopeptides.

11 (previously presented). A method according to claim 10, wherein some but not all of said hydroxyl groups are removed

during said deprotection step.

12-15 (cancelled).

16 (withdrawn). A method according to claim 1, wherein said core peptide comprises tandem repeats.

17 (previously presented). A method according to claim 1, wherein each glycosylation site on said core peptide is unique and distinguishable from other sites due to the identity of the amino acid providing said glycosylation site and the identities of the immediately adjacent amino acids.

18 (cancelled).

19 (original). A method according to claim 1, wherein said glycosylation sites provide hydroxy functions for O-glycosylation or carboxy or carboxamido functional groups for N-glycosylation.

20 (previously presented). A method according to claim 44, wherein said glycosylation sites of said unglycosylated peptides include one or more of serine, threonine, hydroxylysine and asparagine.

21 (previously presented). A method according to claim 44, wherein said glycosylation sites of said unglycosylated peptides consist entirely of d-optical configuration.

22 (previously presented). A method according to claim 1, wherein said core peptide is constructed entirely of d-amino acids.

23 (original). A method according to claim 1, wherein said core peptide is linear.

24 (withdrawn). A method according to claim 1, wherein said core peptide is cyclic.

25 (withdrawn). A method according to claim 1, wherein said glycopeptide comprises a UV-active or fluorescent label.

26 (previously presented). A method according to claim 1, wherein said core peptide comprises hydrophobic amino acids which increase the solubility of the peptide in organic solvents.

27 (previously presented). A method according to claim 44,

wherein said glycosylation sites of said unglycosylated peptides are spaced, singly or in clusters, between sequences that include hydrophobic amino acids.

28 (withdrawn). A method according to claim 1, wherein said glycopeptides comprise lipid chains.

29 (withdrawn). A method according to claim 1, wherein said glycosyl donors are unnatural.

30 (previously presented). A method according to claim 1, wherein at least one carbohydrate structure of at least one glycopeptide of said library comprises a carbohydrate structures associated with a human cell surface antigen, the latter structure acting as a receptor for a bacterial adhesion ligand.

31 (withdrawn). A method according to claim 1, wherein said glycosyl donors comprise structures associated with malignant cell antigens.

32-41 (cancelled).

42 (previously presented). The method of claim 1 in which the core peptides for all of the glycopeptides provided in step (a) are identical.

43 (previously presented). The method of claim 1 further comprising providing said first level library by (a') glycosylating at least one unglycosylated peptide, said unglycosylated peptide comprising at least one unblocked glycosylation site.

44 (previously presented). The method of claim 43 in which step (a') is a random glycosylation obtained by reacting the unglycosylated peptides with a mixture of at least two different glycosyl donors.

45 (previously presented). The method of claim 42 in which the core peptides for all of the glycopeptides of said first level library are identical.

46 (previously presented). The method of claim 1 wherein all of the members of said second level library are

glycopeptides.

47 (previously presented). The method of claim 1 wherein all of the members of said first level library are glycopeptides.

48 (previously presented). The method of claim 1 wherein said glycosyl donors comprise sialyl.

49 (previously presented). The method of claim 1 wherein at least one core peptide is at least four amino acids long and is derived from a cancer-associated mucin.

50 (previously presented). The method of claim 49 in which at least one core peptide is derived from a MUC1 core protein.

51 (previously presented). The method of claim 1 wherein random glycosylation is achieved in step (b) by reacting the first level library with a mixture of at least three different glycosyl donors.

52 (previously presented). The method of claim 1 wherein random glycosylation is achieved in step (b) by reacting the first level library with a mixture of not more than five different glycosyl donors.

53 (previously presented). The method of claim 1 wherein the glycopeptides of said first level library each present not more than five unblocked glycosylation sites.